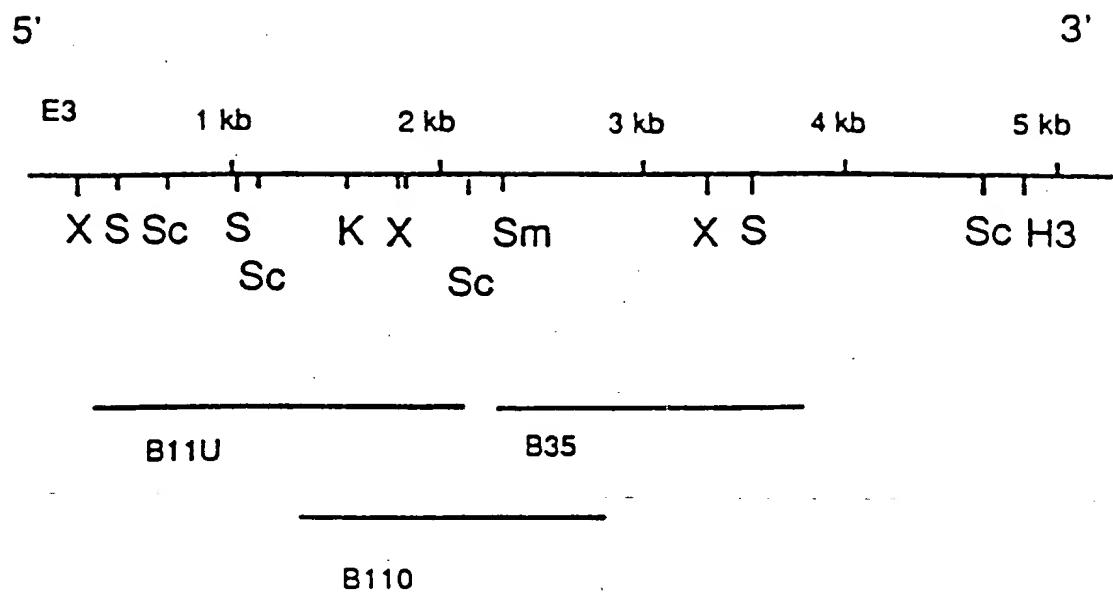


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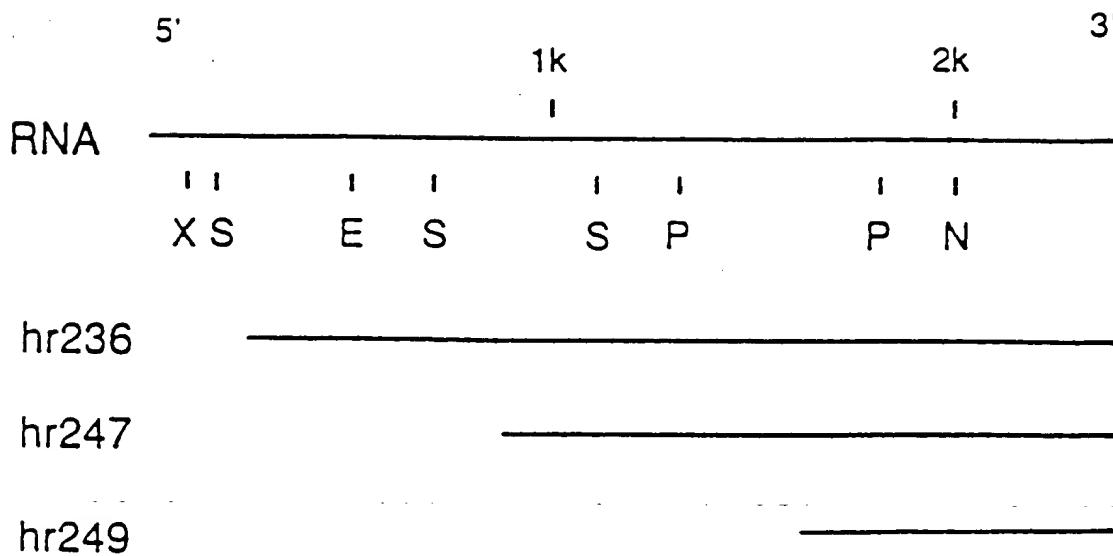
Map of HaSV RNA 1 clones



H3=Hind3, K=Kpn1, Sc=Sac1, S=Sal1, Sm=Sma1, X=Xho1

III-1a.

Map of HaSV RNA 2 clones



E=EcoR1, N=Not1, P=Pst1, S=Sal1, X=Xho1

III. 1b.

3|56

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          10      30      50
GTTCTGCCCTCCCCGGACGGTAAATAAGGGAACAAATGTTACCGGAAAGCGACAGACGTG
          70      90      110
GGCGGTGTCTACGCCGGCAGATGTCGCCTACCGGAAACGTTACTGCAGGAGCCAGTC
          130     150     170
AAGTTGGACTTGGCCGGCACTGAAAGGCCACTAGAAACCCCTCCACAGACTGTACTATCCG
          190     210     230
CTGGCTTCAAAGGGGCACCTTACCCCCGACACAACACCCGATCCTGGCCGGCACCAA
          250     270     290
CGTGTGGCAGAAGAGGGTCTGCCAACAAATTGCACAGGTAGGCACAGTGCCTCGAGATA
          300     320     340
R V A E E V L H N F A R G R S T V L E I

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2.1

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4/56

310 GGCCCGTCTGCACAGCGCACTTAACGCTACATGGGGCACCGAACGCCCGTCGAGAC	330 G P S L H S A L K L H G A P N A P V A D	3.50
370 TATCACGGGTGCACCAAGTACGGCACCCGGGACGGCTTCGGGACACATTACGGCCCTTAGAG	390 Y H G C T K Y G T R D G S R H I T A L E	410
430 TCTAGATCCGGTCCGCCACAGGGCCGGAGTTCAAGGGCCGACGCCCTCACTGCTGCCAAC	450 S R S V A T G R P E F K A D A S L L A N	470
490 GGCATTGCCCTCCGGCACCCCTCTGCGTCTGGCTCGAGTCGGCTCTTGCAGCTCAAATCGCGC	510 G I A S R T F C V D G V G S C A F K S R	530
550 GTTGGAATTGCCAATCACTCCCTCTATGACGTTGACCCCTAGAGGAGCTGGCCAATGCGTTT		590

三 2.2

D G E C G C T T C G G A C C A G G D

610 630 650
GAGAACCGGAACTTCACATGGTCCGGCGTTCATGGCACATGCCAGAAGAGCTGCTCTAC
-----+-----+-----+-----+-----+-----+
E N H G L H M V R A F M H M P E E L L Y

670 690 710
ATGGACAAACGGTGGTTAATGCCCGAGCTCGGCTTACCGCTTACGTTATGAAAGAGCCATATG
-----+-----+-----+-----+-----+-----+
M D N V V N A E L G Y R F H V I E E P M

730 750 770
GCTGTGAAGGAACTGGCCATTCCAGGGGGGGACCTCCGTCTCCACTTGAGTTGGAC
-----+-----+-----+-----+-----+-----+
A V K D C A F Q G G D L R L H F P E L D

790 810 830
TTCATCAACGAGGCCAAGAGCCGGCATCGAGAGGCTGGCCGCCGGCTCCTACTCC
-----+-----+-----+-----+-----+-----+
F I N E S Q E R R I E R L A A R G S Y S

850 870 890
AGACGGCCGCGTCAATTCTCCGGCGACGACTGGGGTGAATGCGTACTTACACGACTTC
-----+-----+-----+-----+-----+-----+
R R A V I F S G D D W G D A Y L H D F

III. 2.3

5/56

910 930 950
CACACATGGCTTGCCTTACCTTACTGGTGAGGAAC"TTACCCACTCCGT"TTGGTTTCTCACTC
- - - + - + - + - + - + - + - + - + - +
H T W L A Y L L V R N Y P T P F G F S L

970 990 1010
CATATAGAAGTCCAGAGGCCAACGGCTCCAGGATTGAGGCTCGGCATCACTCGGCCATCGGCCA
- - - + - + - + - + - + - + - + - + - +
H I E V Q R R H G S S I E L R I T R A P

1030 1050 1070
CCTGGAGACCCATGCTGGCGTCCAGGACGGTCCAAAGGACGGCTCTGCAGAAATCCCA
- - - + - + - + - + - + - + - + - + - +
P G D R M L A V V P R T S Q G L C R I P

1090 1110 1130
AACATCTTTATTACGCCGACGGTCCGGCACTGAGGATAAGACCATTACGTCACAG
- - - + - + - + - + - + - + - + - + - +
N I F Y A D A S G T E H K T I L T S Q

1150 1170 1190
CACAAAGTCAACATGCTCAATTATTGCAAACGGCTCCTGAGAAGGAACTAGTCGAC
- - - + - + - + - + - + - + - + - + - +
H K V N M L L N F M Q T R P E K E L V D

III. 2.4

1210 1230 1250
 ATGACCGTCTGTGATGTCGTGGGGCTAGGCTGGGGGAATCGTGGTCGGCTCAGAA
 - +-----+ +-----+ +-----+ +-----+ +-----+ +-----+
 M T V L M S F A R A R L R A I V V A S E

1270 1290 1310
 GTCAACCGAGGCTCCCTGGAACATCTCACCGGCTGACCTGGCTGGCACACTGTCGTCCTT
 - +-----+ +-----+ +-----+ +-----+ +-----+ +-----+
 V T E S S W N I S P A D L V R T V V S L

1330 1350 1370
 TACGGCTCCACATCATCGACGGGGGAAGGGCTGGGGCTGGCTGTCAGACGCCAAGGAC
 - +-----+ +-----+ +-----+ +-----+ +-----+ +-----+
 Y V L H I I E R R A A V A V K T A K D

1390 1410 1430
 GACGGTCTTGAGAGACTTCGTTCTGGAGAGTCTCAAGCACGTCTGGGCTTCCTGTTGC
 - +-----+ +-----+ +-----+ +-----+ +-----+ +-----+
 D V F G E T S F W E S L K H V L G S C C

1450 1470 1490
 GGTCTGGCAAACCTCAAAGGCACCGACGTCGTCGTTACTAAGCGCGTCAAGTAC
 - +-----+ +-----+ +-----+ +-----+ +-----+ +-----+
 G L R N L K G T D V V F T K R V V D K Y

1510 1530 1550
 CGAGTCCACTCGCTCGGAGACATAATCTGGACGCTCCGCCCTGAAACAGGTCCGGC
 -+-----+-----+-----+-----+-----+-----+
 R V H S L G D I I C D V R L S P E Q V G

1570 1590 1610
 TTCCCTGCCGTTCCGGTACCCACCTGCCGGTCTTCAACGACAGGGAAAGAGCTTGAGGGTC
 -+-----+-----+-----+-----+-----+-----+
 F L P S R V P P A R V F H D R E E L E V

1630 1650 1670
 CTTGCCGAAGCTGGCTTACAACGAAACGGTCCGGTACCTTCCACTCCCTGTGGAGGGAG
 -+-----+-----+-----+-----+-----+-----+
 L R E A G C Y N E R P V P S T P P V E E

1690 1710 1730
 CCCCAAGGTTTCGACGCCGACTTGTGGCACGGCACGGGCCCTCACTCCCCGAGTACCGC
 -+-----+-----+-----+-----+-----+-----+
 P Q G F D A D L W H A T A A S L P E Y R

1750 1770 1790
 GCCACCTTGCAGGGCAGGTCTCAACACCCGACGTCAGGCTCAAGATCACCCCTCGAGAAC
 -+-----+-----+-----+-----+-----+-----+
 A T L Q A G L N T D V K Q L K I T L E N

1810 1830 1850
 GCCCTAAGACCATCGACGGCTCACCCCTCTCCCAAGTCAGAGGCCCTCGAGATGTACGAG
 - +-----+-----+-----+-----+-----+-----+-----+
 A L K T I D G L T L S P V R G L E M Y E

1870 1890 1910
 GGCCCCGCCAGGGCAAGACGGCACCCCTCATGCCGCCCTTGAGGCCGCCGCC
 - +-----+-----+-----+-----+-----+-----+-----+
 G P P G S G K T G T L I A A L E A A G G

1930 1950 1970
 AAAGCACTTTACGTGGCACCCACCAGAGAACTGAGAGGGCTATGGACCGGGATCAA
 - +-----+-----+-----+-----+-----+-----+-----+
 K A L Y V A P T R E L R E A M D R R I K

1990 2010 2030
 CGGGCGCCCTCGGCTACGCAACATGTCGCCCTTGGGATTCTCCGTCGTGCCACCGCC
 - +-----+-----+-----+-----+-----+-----+-----+
 P P S A S A T Q H V A L A I L R R A T A

2050 2070 2090
 GAGGGCCCTTTCGCTACCGTGGTTATCGAGCTCATGTTCCCGCTCGTGTAC
 - +-----+-----+-----+-----+-----+-----+-----+
 E G A P F A T V V I D E C F M F P L V Y

9/56

III. 27

2110 2130 2150
 GTCGGGATCGTGCACGGCTTGTCCCCGAGCTACGAATTAGTCCTTAGGGGACGTTCCAC
 -+-----+-----+-----+-----+-----+-----+-----+
 V A I V H A L S P S S R I V L V G D V H

 2170 2190 2210
 CAAATCGGGTTATAGACTTCCAGGCACAAGGGCAACATGCCGGCACGTC
 -+-----+-----+-----+-----+-----+-----+-----+
 Q I G F I D F Q G T S A N M P L V R D V

 2230 2250 2270
 GTTAAGCAGTGGCGTCAACCAAACCAAGGGCTGTGGCCGGGGGACGTT
 -+-----+-----+-----+-----+-----+-----+-----+
 V K Q C R R T F N Q T K R C P A D V V

 2290 2310 2330
 GCCACCACGTTTCCAGAGCCTTGTAACCCGGGTGCACAAACACCTCAGGGTGGCGCA
 -+-----+-----+-----+-----+-----+-----+-----+
 A T T F F Q S L Y P G C T T S G C V A

 2350 2370 2390
 TCCATCAGCCACGTCGCCAGACTAACGGCAACAGCCAGGGCAAACGCTCTGCTTCACG
 -+-----+-----+-----+-----+-----+-----+-----+
 S I S H V A P D Y R N S Q A Q T L C F T

10/56

III. 2.8

2410 2430 2450
 CAGGAGAAAAGTCGGCCACGGGCTGAGGGCGATGACTGTGCACGGCAAGGGA
 -+-----+-----+-----+-----+-----+-----+
 Q E E K S R H G A E G A M T V H E A Q G

 2470 2490 2510
 CGCACTTTGGCTCTGCAATTCTGCATTACAACGGCTCCACAGCAGAACGCTCCTC
 -+-----+-----+-----+-----+-----+-----+-----+
 R T F A S V I L H Y N G S T A E Q K L L

 2530 2550 2570
 CCTGAGAAGTCGGACCCCTTAAGTCGGCATTCACGCCACACCAACCAACCTGTACATCCGC
 -+-----+-----+-----+-----+-----+-----+-----+
 A E K S H L L V G I T R H T N H L Y I R

 2590 2610 2630
 GACCCGACAGGTGACATTGAGAGACAACCTCAACCATAGCCGAAAGCCGAGGGTGTTTACA
 -+-----+-----+-----+-----+-----+-----+-----+
 D P T G D I E R Q L N H S A K A E V F T

 2650 2670 2690
 GACATCCCTGCACCCCTGGAGATCACGACTGTCAAACCGAGTGAAGAGGTGCAGGCCAAC
 -+-----+-----+-----+-----+-----+-----+-----+
 D I P A P L E I T T V K P S E E V Q R N

2710 2730 2750
GAAGTGATGGCAACGATAACCCCCGAGACTGCCACGGCACGGAAATCCATCTGCTC
- +-----+-----+-----+-----+-----+-----+
E V M A T I P P Q S A T P H G A I H L L

2770 2790 2810
CGCAAGAACTTGGGGACCAACCCGACTGTGGCTGCTGTTGGCGAAGAACCGGCTAC
- +-----+-----+-----+-----+-----+-----+
R K N F G D Q P D C G C V A L A K T G Y

2830 2850 2870
GAGGTTGTTGGGGTCTGCCAANATCAACGTTAGAGCTTGGCGAACCCGACGGCACCCCG
- +-----+-----+-----+-----+-----+-----+
E V F G R A K I N V E L A E P D A T P

2890 2910 2930
AAGCCGCATAGGGCTCCAGGAAGGGGTACAGTGGGTCAAGGGTCAACGGTCTAAC
- +-----+-----+-----+-----+-----+
K P H R A F Q E G V Q W V K V T N A S N

2950 2970 2990
AAACACCAGGGCTCCAGACGGCTACACCCAAGCGAAGGGCTGACCTGCCG
- +-----+-----+-----+-----+-----+
K H Q A L Q T L S R Y T K R S A D L P

III. 240

3010 3030 3050
 CTACACGAAGCTAAGGAGGACGTCAAACGGCATGCTAAACTCGCTTGACCGACATGGAC
 L H E A K E D V K R M L N S L D R H W D

 3070 3090 3110
 TGGACTGTCACTGAAGACGGCCGTGACCGAGGCTGTCTGGAGCACCCAGCTCAAGTCACC
 W T V T E D A R D R A V F E T Q L K F T

 3130 3150 3170
 CAACGGGGCACCGTGGAGACCTGGCTGGAGCCAGACGACCCCTACATCCGTGACATA
 Q R G G T V E D L L E P D D P Y I R D I

 3190 3210 3230
 GACTTCTTATGAAGGACTCAGCAGAAAGTGTGGCCAAAGCCCCGATCAATAACGGCAAGGTC
 D F L M K T Q Q K V S P K P I N T G K V

 3250 3270 3290
 GGGCAGGGGATCGCCGGCTCACTCAAAGTCTCTCAACTTCTCGTCCGGCTTGGATACGC
 G Q G I A H S K S L N F V L A A W I R

13/56

III - 2.11

3310 3330
ATACTGGAGGATACCTCCGTACCGGGAGGCCGACGGTCCGGTACAGCAACGGTCTCCCC
I L E I L R T G S R T V R Y S N G L P

3370 3390
GACGAAGAGGGCCATGGCTGCTGGAAAGCATCAAGTCCCACACGCCACCGTTC
D E E A M L L E A K I N Q V P H A T F

3430 3450
GTCTGGGGACTGGACCGAGTTTGACACCGGACATAACACGGACTGAGCTGCTTCTTC
V S A D W T E F D T A H N N T S E L L F

3490 3510
GCCGCCCTTTAGGGCATTGGCACGGCTGGCAGGCTTAGGCTTAAATCTTACAGAGAACGG
A A L E R I G T P A A V N L F R E R

3550 3570
TGTGGAAACGCACCTTGGCAGGCAAGGGTCTAGGCTCCGTTGAAGTCGACGGTC'TGCTC
C G K R T L R A K G L G S V E V D G L L

III. 2.12

14/56

3610 3630 3650
 GACTCCGGCAGCTTGGCAACACCATTCTCTGCCGCTCATGCTC
 - +-----+-----+-----+-----+-----+-----+
 D S G A A W T P C R N T I F S A A V M L

3670 3690 3710
 ACGCTCTTCCGGCGCTCAAGTTCCGAGCTTCAAGGCCAACGGACTCGCTCCTCTGTGGT
 - +-----+-----+-----+-----+-----+-----+
 T L F R G V K F A A F K G D S L L C G

3730 3750 3770
 AGCCATTACCTCCGGTTCCGACCGCTTAGCCGCCATTACATGGGGGAACGTTACAAGACCAA
 - +-----+-----+-----+-----+-----+-----+
 S H Y L R F D A S R L H M G E R Y K T K

3790 3810 3830
 CATTGAAAGGTCCGGTGGAAATTGGTGGCGTACATCGGAACTCCGTCTCCGCTGAG
 - +-----+-----+-----+-----+-----+-----+
 H L K V E V Q K I V P Y I G L L V S A E

3850 3870 3890
 CAGGTCCGTCGACCCCTGTCAGGAGCCCTCAAGATAATTGGGGCTACACAAGC
 - +-----+-----+-----+-----+-----+-----+
 Q V V L D P V R S A L K I F G R C Y T S

III. 2/3.

3910 3930 3950
 GAACTCCTTACTCCAAGTACGTTGGAGGCTGTGAGAGACATCACCAAGGGCTGGAGTGAC
 -+-----+-----+-----+-----+-----+-----+-----+
 E L L Y S K Y V E A V R D I T K G W S D

 3970 3990 4010
 GCCCCGCTACCACAGGCCCTCCCTGTGCCACATGTCAGGCATGCTACTACAATTACGGCGGGAG
 -+-----+-----+-----+-----+-----+-----+-----+
 A R Y H S L L C H M S A C Y Y N Y A P E

 4030 4050 4070
 TCTGGGGGTACATCATCGACGGCTGTTGGCTTTCGGGGGCACTTCCCCTTGAA
 -+-----+-----+-----+-----+-----+-----+-----+
 S A A Y I I D A V V R F G R G D F P F E

 4090 4110 4130
 CAACTGGGGTGGTGGCTGCCCATGTCAGGCACCCGACGCCATTACAGCAGCACGTATCCG
 -+-----+-----+-----+-----+-----+-----+-----+
 Q L R V V R A H V Q A P D A Y S S T Y P

 4150 4170 4190
 CCTAACGGTGGCCGATCGTGGCTTTCGACCCACGTTCTGAGCCCCGCCAGGGGGGGGG
 -+-----+-----+-----+-----+-----+-----+-----+
 A N V R A S C L D H V F E P R Q A A A P

16/56

III. 2.14

4210 4230 4250
 GCAGGTTTCGTGCCACATGGTGGAAAGCCGAAACGGCTTCTTCACTTACCGGAAAGCT
 - - - + - - - + - - - + - - - + - - - + - - - + - - - +
 A G F V A T C A K P E T P S S L T A K A
 M C E A G N A F F T Y R E S W
 P11a start 4290 4310
 4270 4290 4310
 GGTGTTCTGCCACTACAAGCCACCGTTGGACTGGACTGGGACTTGCGCCCCGGAGTCTCCATGG
 - - - + - - - + - - - + - - - + - - - + - - - + - - - +
 G V S A T T S H V A T G T A P P E S P W
 C F C D Y K P R C D W D C A P G V S M G
 4330 4350 4370
 GATGCACCTGCCAGAACAGCTTTCTGGAGTTATTGACACGGAGACCCCCGTCCACATCA
 - - - + - - - + - - - + - - - + - - - + - - - +
 D A P A N S F S E L L T P E T P S T S
 C T C S Q Q L F G V I D T G D P V H I I
 4390 4410 4430
 TCCTCGCCGTCATCGTCTCATCGGACTCTCTACATCGTGTGGAAAGGTCTCAGTGGT
 - - - + - - - + - - - + - - - + - - - + - - - +
 S S P S S S S D S S T S C G R S L S G
 L A V I V F I G L L Y I V W K V A Q W W

17|56

III-2.15

4450 4470 4490
GGAGACACCGCAAGGACCAACAGAACACTTGAACAGCAGAAAGCCGCCCTTCGCAAGACAGG
- + - + - + - + - + - + - + - + - + - + - +
G D T A R T T E D L N S R K P P S Q D R
R H R K D H R R L E Q Q K A A F A R Q A

18/56

4510 4530 4550
CAATCACGCTCTGAATGTCTGGACAGAAGGGAGAAAGGACAGGCAGTTCGTTAACT
- + - + - + - + - + - + - + - + - + - + - +
Q S R S S E C L D R S G E R T G S S L T
I T L V * M S G Q K R R K D R Q F V N C
P11b start

4570 4590 4610
CCCCCACTGCTCCGAGCCCTCATTTCTCGAAAGAGCTCGACTGGCGACCGGG
- + - + - + - + - + - + - + - + - + - +
A P T A P S P S F S F S E R A R L A T G
P H C S E P L I L I F G K S S T G D R A

4630 4650 4670
CCGACTGTCGCCGCTGGACATCACCTCGGAAACCCCATCCTGGCCACGGACAGGTT
- + - + - + - + - + - + - + - + - + - +
P T V A A T S P S A T P S C A T D Q V
D C R R C D I T F G N P I L R H G P G C

III. 2.16

4690 4710 4730
 GCCGGAGGACCCGGAACTTGCGCCCTTGGGTTCCTGCCAGTCTGCCGTCGCTGTC
 +-----+-----+-----+-----+-----+-----+
 A A R T T P D F A P F L G S Q S A R A V
 R E D H A G L C A F P V C P V C C L

 4750 4770 4790
 TCGAAGGCCGTACCGGGCCCCCACGAACTGCCGTTGGAAAGAAAGTCACCCCGCTCCACGCC
 +-----+-----+-----+-----+-----+-----+
 S K P Y R P P T T A R W K E V T P L H A
 E A V P A P H D C P L E R S H P A P R V

 4810 4830 4850
 TGGAAAGGGCGTACCGGGAGACCGAACCGAACGGAAAGTCAGGCAGGACCCCCGGAGACAGGGCGGCC
 +-----+-----+-----+-----+-----+
 W K G V T G D R P E V R E D P E T A A V
 E G R D R R P T G S Q G G P G D S G G R

 4870 4890 4910
 GTCCAGGGCTCTGATCAGCGGGCGTTATCCTCAGAAAGACGAAGGCTTCCCTCCGACGCCATCC
 +-----+-----+-----+-----+-----+
 V Q A L I S G R Y P Q K T K L S S D A S
 P G S D Q R P L S S E D E A F L R R I Q

19/56

III-217

4930 4950 4970
 AAAGGCTACTCAAGAACTAAGGGATGCTCACAAATCCACCCCTCTTCTGCCCGAGGTGCG
 K G Y S R T K G C S Q S T S F P A P S A
 R L L K N * M L T I H L F S C P E C G
 P14 start 5030
 4990 5010 5030
 GATTACCAGGGCCCCGGACTGCCAGACAGTCAGTCTGCCGGCCGCTGCAGAGATGGCG
 D Y Q A R D C Q T V R V C R A A E M A
 L P G P R L P D S P S L P R R C R D G A
 5050 5070 5090
 CGCTCATGTATTCACCGAGCCGTTGGCTCATCTGCCGCCAGTGCCTGAAGGCCATA
 R S C I H E P L A S S A A S A D L K R I
 L M Y S R A V G F I C R Q C R L E A H T
 5110 5130 5150
 CGCTCTACCTCGGACTCTGTTCCCGATGTAAAGATCAGCAAGAGCCATGAAGGAAACAAA
 R S T S D S V P D V K I S K S A *
 L Y L G L C S R C K D Q Q E R M K E Q N

2000 1500 1000 500

21/56

5170 5190 5210
ATTAGTTCTTGTAAACAAAGGTGGTCCCTCCATTGAGGTAAAGACTCTGGTGAG
-----+-----+-----+-----+-----+-----+-----+

*

5230 5250 5270
TCCTCAACGTTACTCGTTGAGTCTGCTGCCGTTCGATTCCAAAGCAGCAAAGGGT
-----+-----+-----+-----+-----+-----+-----+

5290 5310
GGGCAACTAGTACGGGGCCCTGGGATACCA
-----+-----+-----+-----+

III. 2.19.

22/56

10 30 50
GTTTTCTTCTTACCAAGTGTGGTAAATTAAACAAAAGAAGAAAACCAGGACCGTAA
-----+-----+-----+-----+-----+-----+-----+

70 90 110
CCGGCCCTTACACACTCTCGAGAGTCGAGTCCGTGACCAACGGATTATACTGTCGCCAACACGGC
-----+-----+-----+-----+-----+-----+-----+

130 150 170
GCCTTTCCGACCACTCTCGAGAGTCGAGTCCGTGAGGACTTTCGTCGGTGAACCAACCCGGTTGGCA
-----+-----+-----+-----+-----+-----+-----+

190 210 230
GTCGACAGCGCTTCCGGACCACTAGAACCTCCTCGAGCGACGGCACACAGGCACACACA
-----+-----+-----+-----+-----+-----+-----+

250 270 290
CGGCCCTTAGCTGCACCTACGGCAGCGTTGATAGCCGGATTATGAGCGAGCACACCATC
-----+-----+-----+-----+-----+-----+-----+
M S E H T I
P17 start

310 330 350
GCCCACTCCATTACACCCGGTACACCCCTTGCCTATAACCCCTGAAACCTGAA
-----+-----+-----+-----+-----+-----+-----+
A H S I T L P P G Y T L A L I P P E P E

III-3a.1

23/56

370 390 410
 GCAGGATGGAGATGCTGGAGTCACAGCGACTCACAAACCGTCAACGGGAACCCGTA
 - +-----+-----+-----+-----+-----+
 A G W E M L E W R H S D L T T V A E P V
 M G D A G V A S Q R P H N R R G T R N
 P71 start 430 450 470
 ACGTTGGGTCAAGGCCAACACCCGTCACCGTCAATGGTAGAAGAAACCAACGGGTCGGA
 - +-----+-----+-----+-----+-----+
 T F G S A P T P S P S M V E E T N G V G
 V R V S A N T V T V N G R R R N Q R R R T
 510 530 550 570 590
 CCGGAAGGCAAGTTCTCCCCCTGACAATTCAACCGCTGCACAAAGACCTCGCCCAA
 - +-----+-----+-----+-----+-----+
 P E G K F L P L T I S P L L H K T S R K
 G R Q V S P P D N F T A A A Q D L A Q S
 L D A N T V T F P A N I S S M P E F R N

III-3a.2

24/56

610 630 650
 ATTGGCCAAGGGAAAGATCGACCTCGACTCCGATTCCCATCGGCTGGTACTTCAGTACC
 +-----+-----+-----+-----+-----+
 I G P R E R S T S T P I P S A G T S S T
 W A K G K I D L D S D S I G W Y F K Y L

670 690 710
 TTGACCCAGGGGTGCTAACAGAGTCTGGCGCCGCTGGCGAGTACTCGAAAGATCCCTG
 +-----+-----+-----+-----+-----+
 L T Q R V L Q S L R A P S A S T R R S L
 D P A G A T E S A R A V G E Y S K I P D

730 750 770
 ACGGCCTCGTCAAGTTCTCGTCCGACGGCAGAGATAAGAGAGATCTATAACGAGGAGTGCC
 +-----+-----+-----+-----+-----+
 T A S S S P S T Q R *
 G L V K F S V D A E I R E I Y N E E C P

790 810 830
 CGGTCTCACTGACCGTGTCCGTCCCCCTCGACGGCCGCCAGTGGAGCCTCTCGATTTCT
 +-----+-----+-----+-----+
 V V T D V S V P L D G R Q W S L S I F S

 \overline{III} .3a.3

00000000000000000000

850 870 890
CCTTCCGATGTTAGAACCGCCTACGTCGCCGTAGCGAACGTCGAGAACAGGAGATGT
- - + - + - + - + - + - + - + - + - +
F P M F R T A Y V A V A N V E N K E M S

910 930 950
CGCTCCGACGGTCAAACGACCTCATCGAGTGCGCTCAACAAATCTGCCGACTGGCGTTATG
- - + - + - + - + - + - + - + - + - +
L D V V N D L I E W L N N L A D W R Y V

970 990 1010
TCGTTGACTCTGAACACAGTGGATTAACTTACCAATGACACCACCGTACTACGTCCGCATCC
- - + - + - + - + - + - + - + - + - +
V D S E Q W I N F T N D T T Y Y V R I R

1030 1050 1070
CGCGTTCTACGTCACCTAACGACGTTCCAGACCCCCACAGGGCCTTGTTCGCACAGTCT
- - + - + - + - + - + - + - + - + - +
V L R P T Y D V P D P T E G L V R T V S

1090 1110 1130
CAGACTACCGCCTCACTTATAAGGGATAACATGTGAAGCCAACATGCCAACACTCGTCG
- - + - + - + - + - + - + - + - + - +
D Y R L T Y K A I T C E A N M P T L V D

III-3a.4

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1150 1170 1190
ACCAAGGCTTTGGATCGGGCCAGTACGGCTCACCCGACTAGCCTACCGCAGTACG
+-----+-----+-----+-----+-----+
Q G F W I G Q Y A L T P T S L P Q Y D

1210 1230 1250
ACGTCAGCGAGGCCAACGCTCTGCACACTTTGACCTTGCACAGCACCATTGCAGGCCGCTG
+-----+-----+-----+-----+-----+
V S E A Y A L H T L T F A R P S S A A A

1270 1290 1310
CACTCGCGTTGTGGCAGGGTACGGGTGGCACAGGGTGGCACTGGCCTGCAGGCACCTCCAG
+-----+-----+-----+-----+-----+
L A F V W A G L P Q G G T A P A G T P A

1330 1350 1370
CCTGGGAGCAGGCATCCTCGGGTGGCTACCTCACCTGGCCACACGGTACTACTTTC
+-----+-----+-----+-----+-----+
W E Q A S S G G Y L T W R H N G T T F P

1390 1410 1430
CAGGCTGGCTCCGTTAGCTACGTTCTCCCTGAGGGTTTGCCCCCTTGAGGGCTACGACCCGA
+-----+-----+-----+-----+-----+
A G S V S Y V L P E G F A L E R Y D P N

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III-3a5

D G E C C T E S S G C C S G D

1450 1470 1490
ACGACGGCTCTGGACCCGACTTTCCGGCAGGAGACACCGTCACTTTCCGGCAGGTGCG
- + - + - + - + - + - + - + - +
D G S W T D F A S A G D T V T F R Q V A

1510 1530 1550
CCGTGACGGAGCTCGTTGACCAACACCCCCGCCGGCGGCAGGGCCCCCACCTTCA
- + - + - + - + - + - + - + - +
V D E V V T N N P A G G S A P T F T

1570 1590 1610
CCGTGAGAGTGGCCCCCTTCAAACCGCTTACACCAACACCCGTTGCTGTTAGAACACCGCTCTTAG
- + - + - + - + - + - + - + - +
V R V P P S N A Y T N T V F R N T L L E

1630 1650 1670
AGACTCGACCCCTCCCTCTCGTAGGCTCGAAGACTCCCTATGCCACCTGCTGACTTTGGACAGA
- + - + - + - + - + - + - + - +
T R P S S R R L E L P M P A D F G Q T

1690 1710 1730
CGGTGGCCAAACCCGAAGATCCGAGCAGTCGCTTCTTAAGAAACACTTGCTGCTATT
- + - + - + - + - + - + - + - +
V A N N P K I E Q S L L K E T L G C Y L

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III. 30.6

1750 1770 1790
TGGTCCACTCCAAATGCCAACCCCCGTTTCCAGCTCACGCCAGCCAGCTCCTTGGCG
-----+-----+-----+-----+-----+-----+
V H S K M R N P V F Q L T P A S S F G A

1810 1830 1850
CCGTTTCCCTCAACAAATCCGGTTATGAGCGCACACCCGACCTCCGGACTACACTGGCA
-----+-----+-----+-----+-----+-----+
V S F N N P G Y E R T R D L P D Y T G I

1870 1890 1910
TCCGTGACTCATTGACCAGAACATGTCCACCCGCTGTGGCCCACTTCCGCTCACTCTCCC
-----+-----+-----+-----+-----+-----+
R D S F D Q N M S T A V A H F R S L S H

1930 1950 1970
ACTCCTGCAGTATCGTCACTAAGACCTACCGGCTTGGGAAGGGCTCACGAAACGTCAAACA
-----+-----+-----+-----+-----+-----+
S C S I V T K T Y Q G W E G V T N V N T

1990 2010 2030
CGCCCTTCGGCCAATT CGCGCACGGGGCCTCCTCAAGAATGAGGAGATCCTCTGCCTCG
-----+-----+-----+-----+-----+-----+
P F G Q F A H A G L L K N E E I L C L A

2050 2070 2090
 CCGACGACCCTGGCCACCCGGTCTCACAGGTGTCTAACCCGCCAACTGACAACTTCGGGGGCG
 +-----+-----+-----+-----+-----+-----+
 D D L A T R L T G V Y P A T D N F A A A

 2110 2130 2150
 CCGTTTCTGCCTTCGGCGGAACATGCTGTCCTCCGTGCTGAAGTCGGAGGCAACGTCCCT
 +-----+-----+-----+-----+-----+-----+
 V S A F A A N M L S S V L K S E A T S S

 2170 2190 2210
 CCATCATCAAGTCCGTTGGCGAGACTGCCGTCCGGCTCAGTCGGCCCTCGCGAAGC
 +-----+-----+-----+-----+-----+-----+
 I I K S V G E T A V G A A Q S G L A K L

 2230 2250 2270
 TACCCGGACTGCTAAATGAGTGTACCGGAAAGATTGCCGGCGTGTCCGGCGCCGAG
 +-----+-----+-----+-----+-----+-----+
 P G L L M S V P G K I A A R V R A R A

 2290 2310 2330
 CGCGCCGGCCGGCTCGTGCCTAGTTGCTCGCTCCTGTTCGCCGGTTCGTAAA
 +-----+-----+-----+-----+-----+-----+
 R R R A A R A N *

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III.3a.8

0000000000000000

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2350 2370 2390
ACGGCCGTCCGGCACATTACGGCTTACCCCTAAAGACTCTGGTAGGTCCCCGGTTACA
- - - + - - - + - - - + - - - + - - - + - - - +

2410 2430 2450
CGACGGGTCTGCCGGGTTCGATTCCATCCCAAGGGCAAGGAAGGACGTTAGCTCT
- - - + - - - + - - - + - - - + - - - + - - - +

2470
CGGTCCCTCGGGATACCA
- - - + - - - -

III.3^{a.9}

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370 390 410
GCAGGATGGCAGATGCTGGCACTGGCGTCAACAGGGACCTCACAAACCGTCGGGAACCCGTA
-----+-----+-----+-----+-----+-----+
A G W E M L E W R H S D L T T V A E P V

430 450 470
ACGTTGGGTCAAGGCCAACACCGTCAACGGTCAATGGTAGAAGAAACCAACGGCGTCCGGA
-----+-----+-----+-----+-----+-----+
T F G S A P T P S P S M V E E T N G V G

490 510 530
CCGGAAGGAAAGTTCTCCCCCTGACAATTCAACCGCTGCTGGCACAAAGACCTCGCGCAA
-----+-----+-----+-----+-----+-----+
P E G K F L P L T I S P L L H K T S R K

550 570 590
GCCTTGACGCCAACACCGTCACTTCCCCGCTAACATCTCTAGCATGCCGAATTCGG
-----+-----+-----+-----+-----+-----+
A L T P T P S L S P A N I S S M P E F R

610 630 650
AATTGGCCAAAGGAAAGATCCGACCTCGACTCCGATTCCATCGGCTGGTACTTCAGTAC
-----+-----+-----+-----+-----+-----+
N W A K G K I D L D S I G W Y F K Y

III-3b.2

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| | | |
|-----|--|---|
| 670 | CTTGACCCAGCGGGTGCACAGAGTCTGGCGGCCGTCGGCAGTAGTACTCGAACATCCCT
+-----+-----+-----+-----+-----+-----+-----+ | L D P A G A T E S A R A V G E Y S K I P |
| 690 | +-----+-----+-----+-----+-----+-----+-----+ | |
| 710 | +-----+-----+-----+-----+-----+-----+-----+ | |
| 730 | GACGGCCTCGTCAAGTTCTCCGTGACCCAGAGATAAGAGAGATCTATAACCGAGGA
+-----+-----+-----+-----+-----+-----+-----+ | D G L V K F S V D A E I R E I Y N E E C |
| 750 | +-----+-----+-----+-----+-----+-----+-----+ | |
| 770 | +-----+-----+-----+-----+-----+-----+-----+ | |
| 790 | CCCGTCTGTAAGTGTCCGTCCCCCTCGACCGGCCAGTGGAGCCTCTCGATTTC
+-----+-----+-----+-----+-----+-----+-----+ | P V V T D V S V P L D G R Q W S L S I F |
| 810 | +-----+-----+-----+-----+-----+-----+-----+ | |
| 830 | +-----+-----+-----+-----+-----+-----+-----+ | |
| 850 | TCCCTTCCGATGTTCAAGAACCGCCTACGTCGGCTAGCGAACAGCTCCGAGAACAA
+-----+-----+-----+-----+-----+-----+-----+ | S F P M F R T A Y V A V A N V E N K E M |
| 870 | +-----+-----+-----+-----+-----+-----+-----+ | |
| 890 | +-----+-----+-----+-----+-----+-----+-----+ | |
| 910 | TCGCTCGACGTTGTCAAACGACCTCATCGAGTGGCTCAACAAATCTGGCGACTGGCGTTAT
+-----+-----+-----+-----+-----+-----+-----+ | S L D V V N D L I E W L N N L A D W R Y |
| 930 | +-----+-----+-----+-----+-----+-----+-----+ | |
| 950 | +-----+-----+-----+-----+-----+-----+-----+ | |

III. 3b.3

970 990 1010
GTCGTGACTCTGAACAGTGGATTAACATTCACTTACGTAACCGTCCGGCATIC
+-----+-----+-----+-----+-----+
V V D S E Q W I N F T N D T T Y Y V R I

1030 1050 1070
CGCGTTCTACGTCCAACCTACGACGTTCCAGACCCCCACAGAGGCCACAGTC
+-----+-----+-----+-----+-----+
R V L R P T Y D V P D P T E G L V R T V

1090 1110 1130
TCAGACTACCGCCTCACTTAAAGGGATAAACATGTAAGCCAAACATGCCAACACTCGTC
+-----+-----+-----+-----+-----+
S D Y R L T Y K A I T C E A N M P T L V

1150 1170 1190
GACCAAGGCTTTGGATCGGGGCCAGTACGGCTCTCACCCGACTAGCCTACCGCAGTAC
+-----+-----+-----+-----+-----+
D Q G F W I G G Q Y A L T P T S L P Q Y

1210 1230 1250
GACGTCAAGGGCCTACGGCTCTGCACACTTGGACCTTCGGCAGACCATCCAGGGCGCT
+-----+-----+-----+-----+-----+
D V S E A Y A L H T L T F A R P S S A A

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III-3b.4

1270 1290 1310
GCACTGGGTTCGTGGCAGGGTGGCACAGGGTGCCACTGCCACTGCAGGGACTCCA
-----+-----+-----+-----+-----+-----+
A L A F V W A G L P Q G G T A P A G T P

1330 1350 1370
GCCTGGGAGGAAGGCAATCCTCGGCTAACCTCACCTGGCTAACAAACGGTACTACTTC
-----+-----+-----+-----+-----+-----+
A W E Q A S S G G Y L T W R H N G T T F

1390 1410 1430
CCAGGCTGGCTCCGTCTAGCTAACGTTCTCCCTGAGGGTTCTGCCCTTGAGGCCTACGACCCC
-----+-----+-----+-----+-----+-----+
P A G S V S Y V L P E G F A L E R Y D P

1450 1470 1490
AACGACGGCTCTTGGACCGACTTCGCTTCCGCAGGAGACACCGTCACTTCCGGCAGGTC
-----+-----+-----+-----+-----+-----+
N D G S W T D F A S A G D T V T F R Q V

1510 1530 1550
GCCGTCGACGGAGGTCTGTTGACCAACACCCGGCGGGCAGGGCCCCACCCCTTC
-----+-----+-----+-----+-----+-----+
A V D E V V V T N N P A G G S A P T F

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III 3b.5

DOE OUT "E5922960

1570 1590 1610
ACCGT GAGGT GCC CTT CAAC CGCT TAC ACC AA
- +-----+ +-----+ +-----+
T V R V P P S N A Y T N T V F R N T L L

1630 1650 1670
GAGACT CGAC CCT CCT CGTAG GCT CGA ACT CC
- +-----+ +-----+ +-----+
E T R P S S R R L E L P M P P A D F G Q

1690 1710 1730
ACGGT CGCA ACAC CCC GAAG AT CGAG CAG TCC
- +-----+ +-----+ +-----+
T V A N N P K I E Q S L L K E T L G C Y

1750 1770 1790
TTGGT CCACT CCAA AAT GCG AAAC CCG TT TCC
- +-----+ +-----+ +-----+
L V H S K M R N P V F Q L T P A S S F G

1810 1830 1850
GCC GT TT CCT CAAC CAAT CGGG TT TAT GAG CG
- +-----+ +-----+ +-----+
A V S F N N P G Y E R T R D L P D Y T G

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III-3 b.6.

DEC 20 1995 ESGC 2960

1870 1890 1910
ATCCGTGACTCATTCGACCAAGAACATGTCGCCACCGCTTGCGCCACTTCCGCTCACTCTCC
I R D S F D Q N M S T A V A H F R S L S

1930 1950 1970
CACTCCTGGCACTGCACTAAAGACCTACCAGGGTGGAAAGGGCTCACGAAACGTCAAC
H S C S I V T K T Y Q G W E G V T N V N

1990 2010 2030
ACGGCTTTGGCCAAATTGGCGAACGGCCTCCTCAAGGAATGAGGAGATCCTCTGCCTC
T P F G Q F A H A G L L K N E E I L C L

2050 2070 2090
GCCGACGCCCTGGCCACCCGGTCTCACAGGTGTTCTACCCCCGCCACTGACAACACTTCGGGCC
A D D L A T R L T G V Y P A T D N F A A

2110 2130 2150
GCCGGTTCTGGCTTCTGGCCATGGCATGCTGTCCTGGCTGAGTCGGAGGGCAACGTC
A V S A F A A N M L S S V L K S E A T S

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III-3b.7

00E00T " E592 2960

2170 2190 2210
TCCATCATCAAGTCCGGTGGCGAGACTGGCGTCGGGCTCAGTCCGGCCTCGCGAAG
-+-----+-----+-----+-----+-----+-----+
S I I K S V G E T A V G A A Q S G L A K

2230 2250 2270
CTACCCGGACCTGGCTAAATGAGTGTTACCGAGGAAGATTGCCGGCGGTGTCCGGCGCCGA
-+-----+-----+-----+-----+-----+-----+
L P G L L M S V P G K I A A R V R A R R

2290 2310 2330
GGGGCCCCGGCCGGCTCGTGGCTCCATTAGTTTGCTCGCTCCGTGTTCTCGCCGTTCTCGTAA
-+-----+-----+-----+-----+-----+-----+
A R R A A R A N *

2350 2370 2390
AACGGCGTGGTCCCCCACATTACGGGTACCCCTAAAGACTCTGGTGAGTCCCGTGTAC
-+-----+-----+-----+-----+-----+-----+
A R R A A R A N *

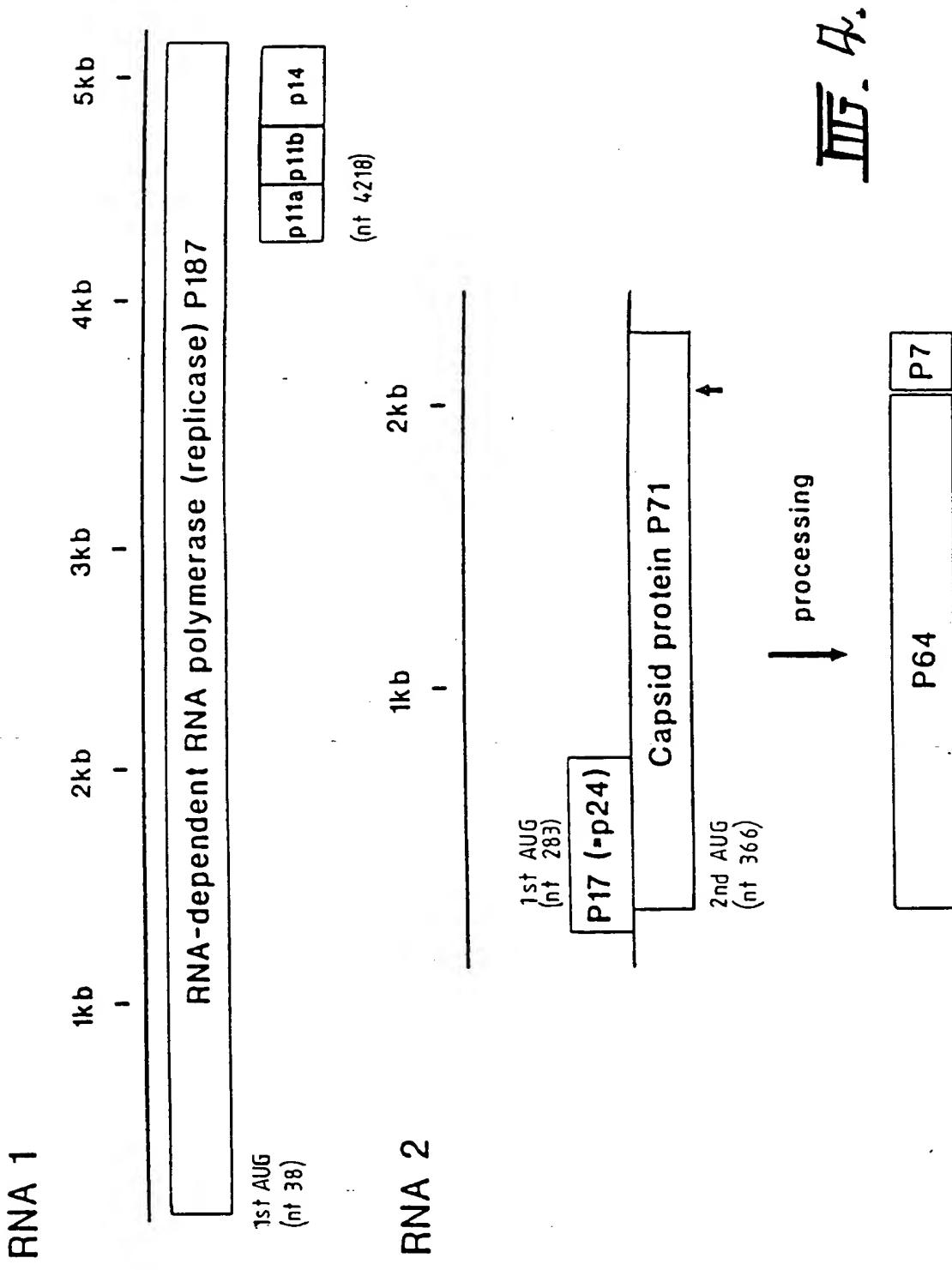
2410 2430 2450
ACGACGGGTCTGCCGGGTTCGATTCCATTCCAAAGGGCAAGAGAACGTTAGTTAGCTC
-+-----+-----+-----+-----+-----+-----+
TGCCTCCCTCGGGATACCA

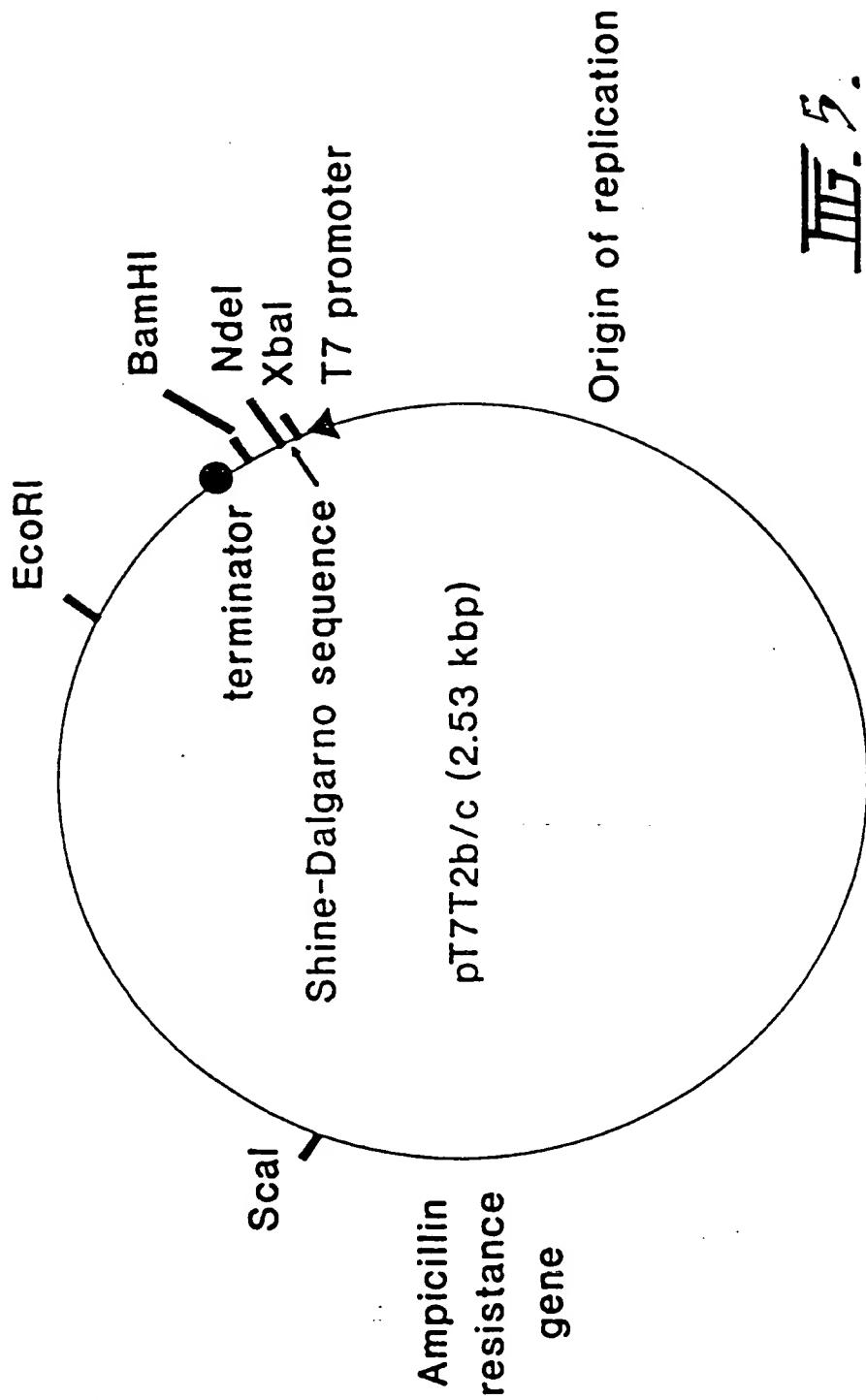
2470
-+-----+-----+

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III. 3b.8

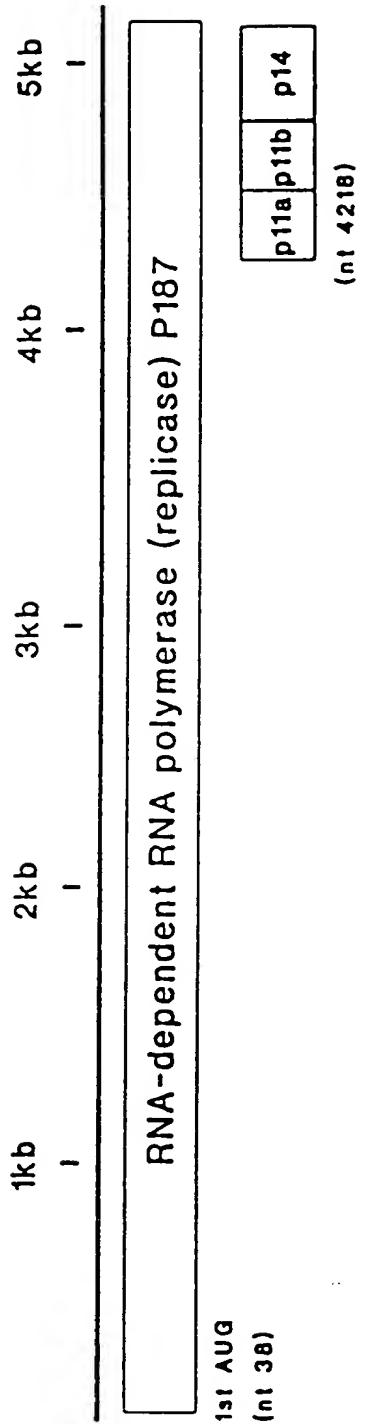
Proteins encoded by the HaSV genome



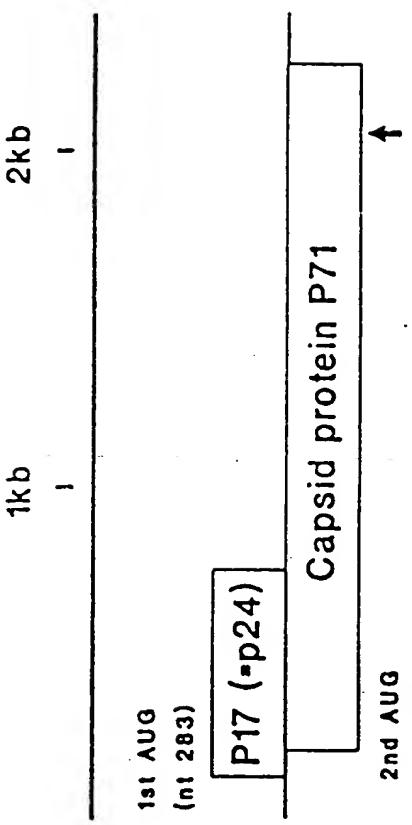


Proteins encoded by the HaSV genome

RNA 1



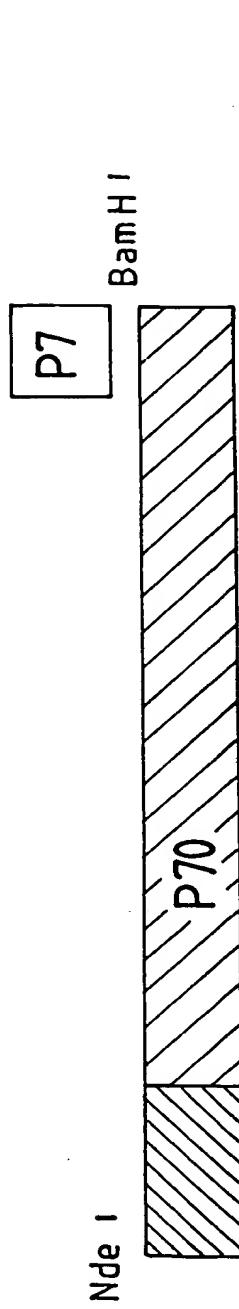
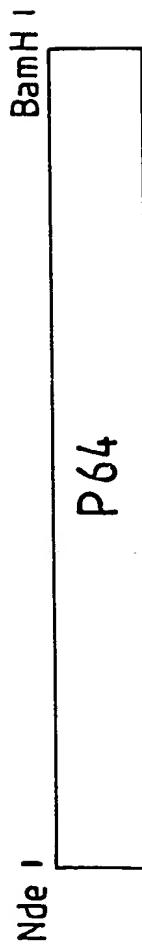
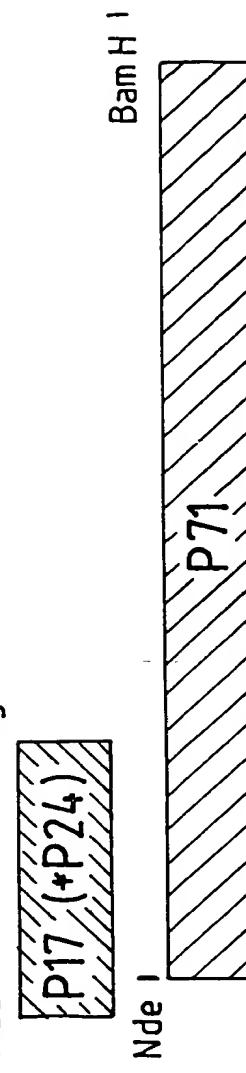
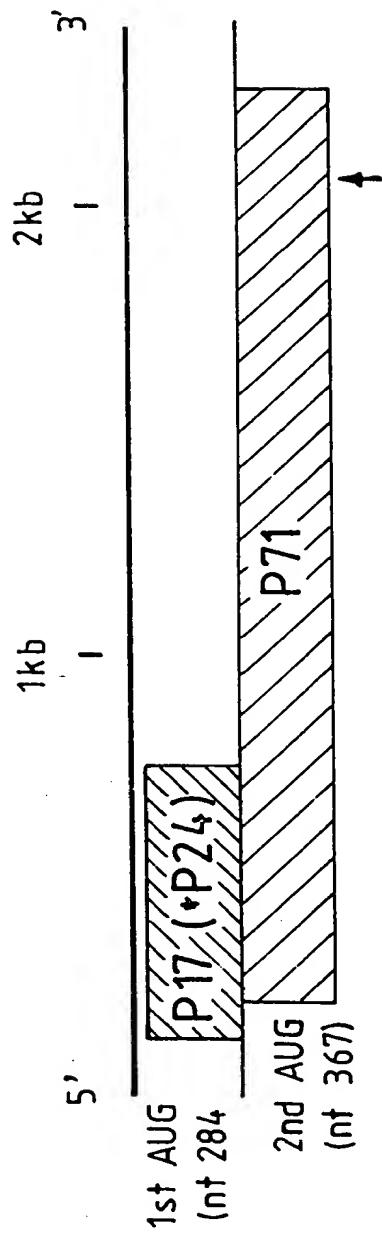
RNA 2



III. 6 -



PROTEINS EXPRESSED FROM HaSV RNA 2



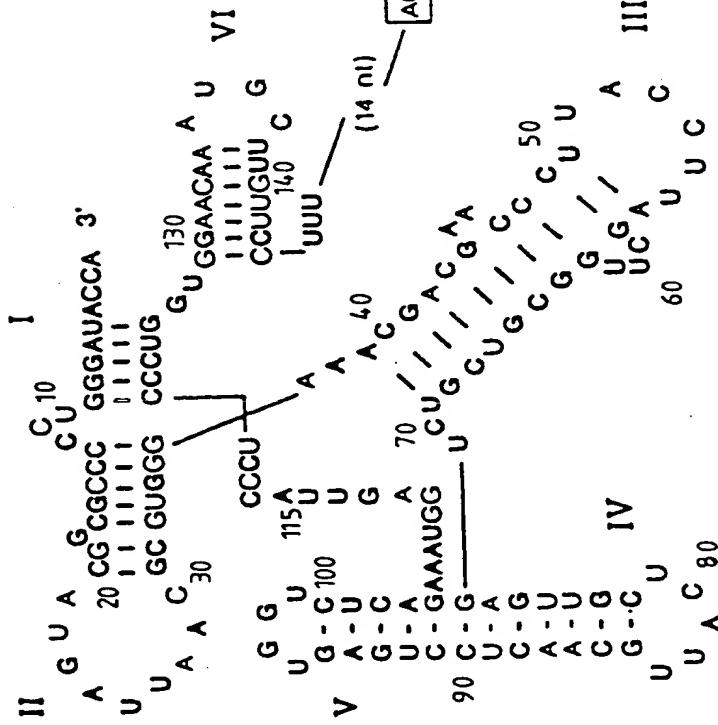
42|56

III. 7.

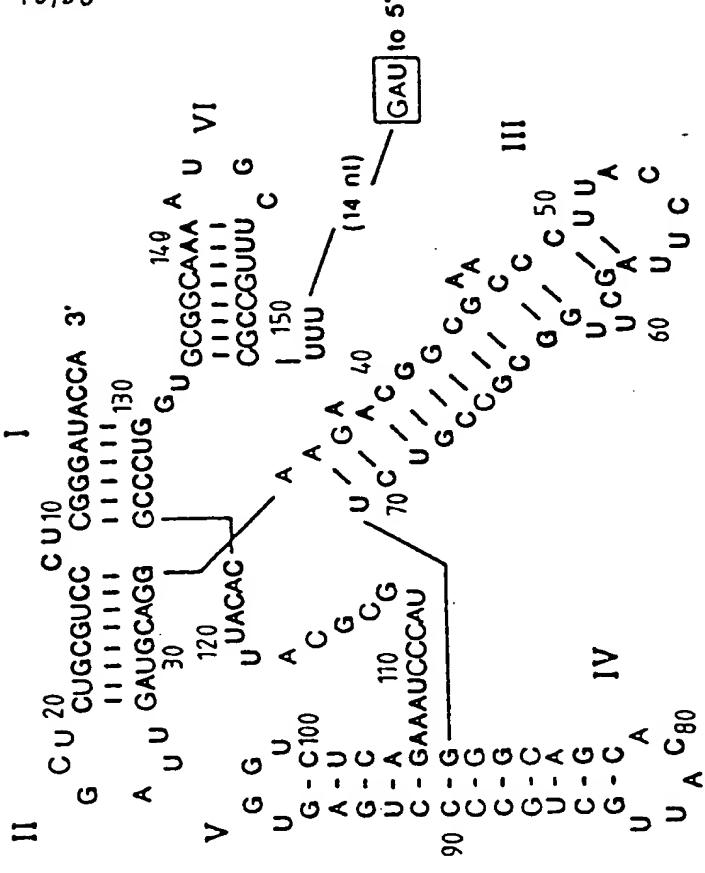
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HaSV RNA 3' - terminal tRNA-like structures

RNA 1



RNA 2



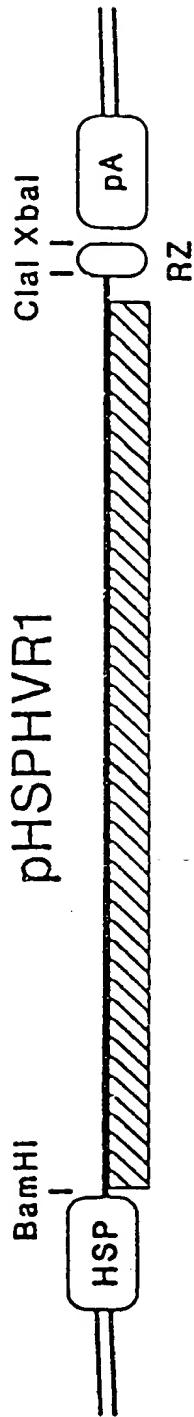
HaSV RNA1



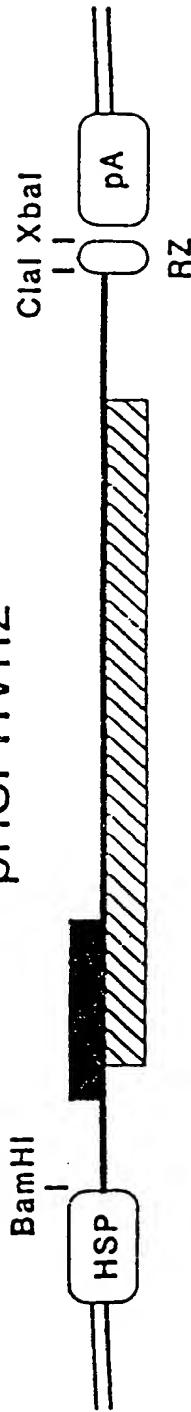
HaSV RNA2



Insect cell expression constructs



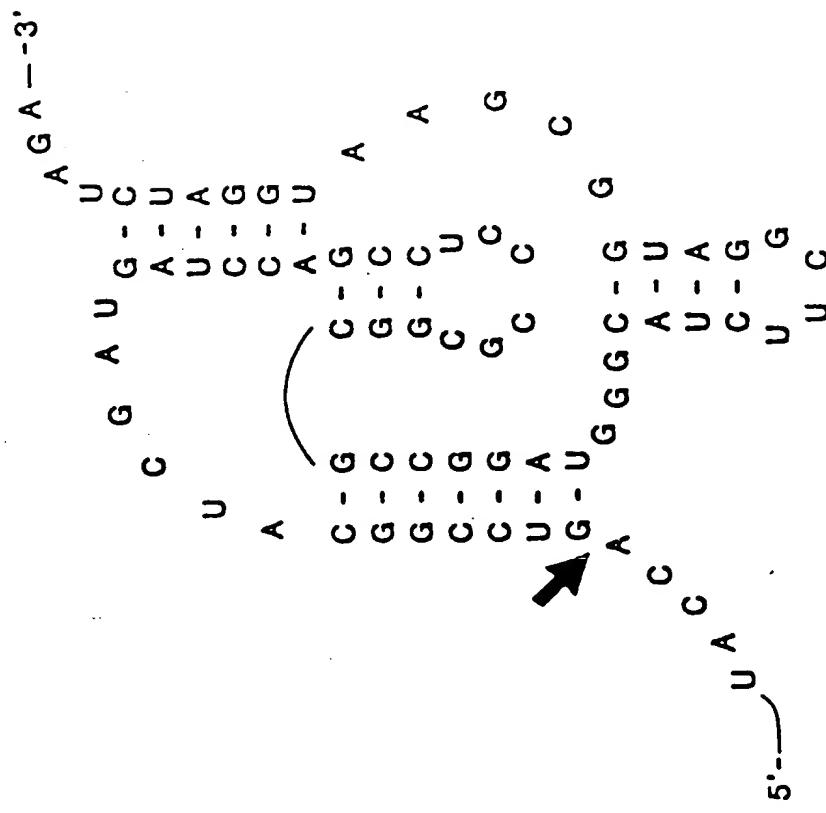
pHSPHVR2



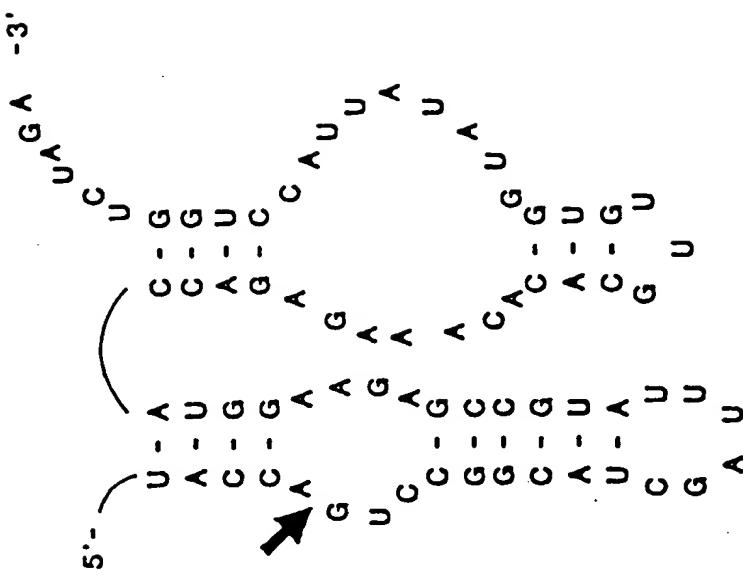
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CIS-ACTING RIBOZYMES FOR HASV 3' ENDS

HEPATITIS DELTA VIRUS



HAIRPIN



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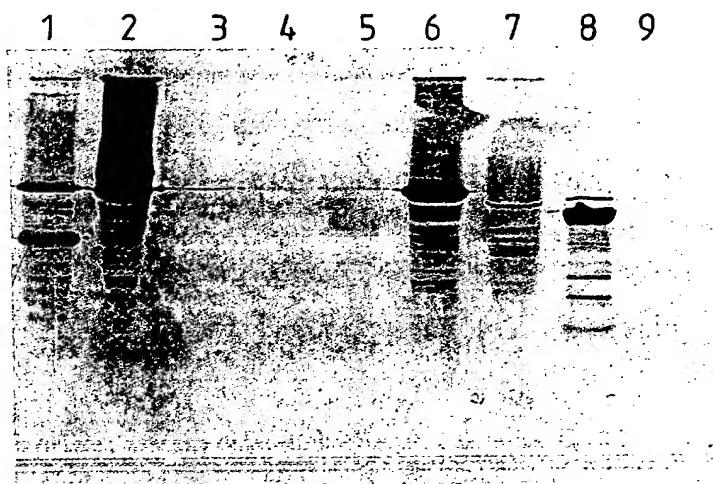
III. 10.

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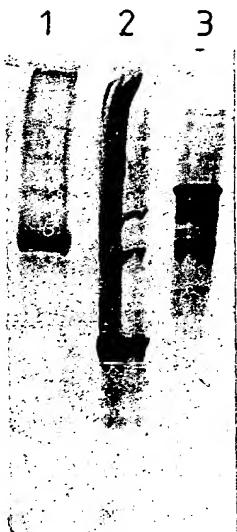
III. 11.

WESTERN BLOTS OF HaSV CAPSID PROTEIN

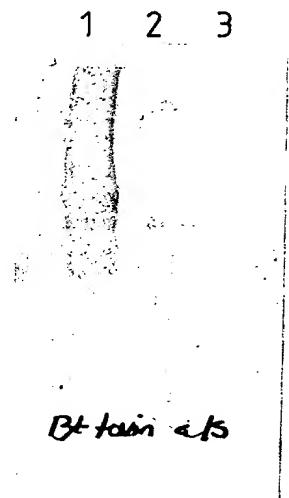
A. HaSV ANTISERUM



B. HaSV ANTISERUM



C. Bt ANTISERUM

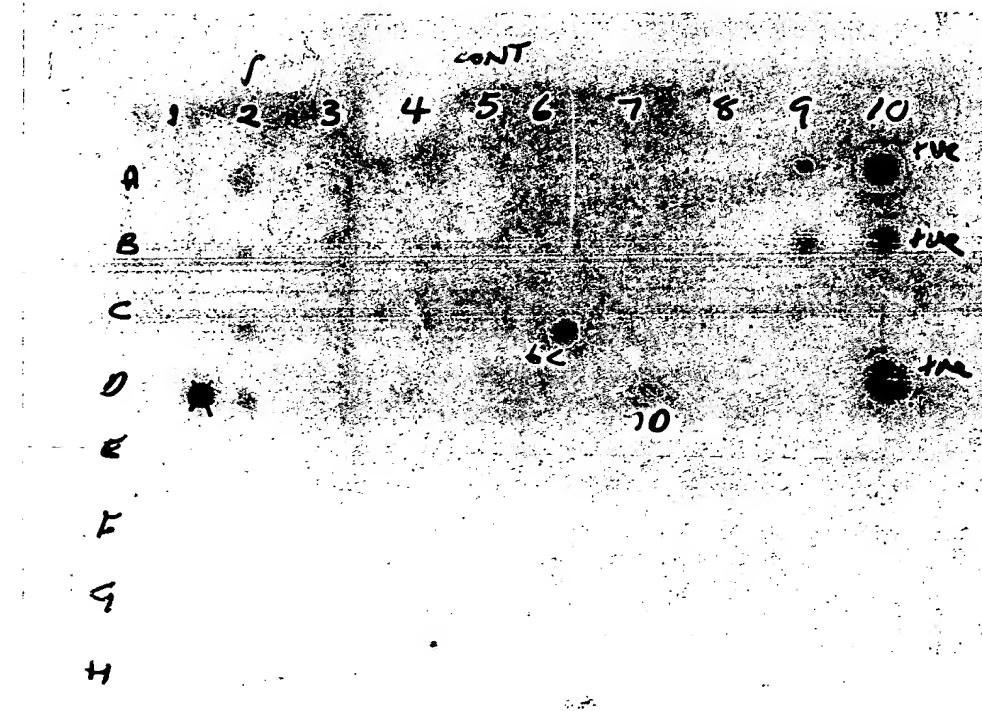


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FIG. 12.

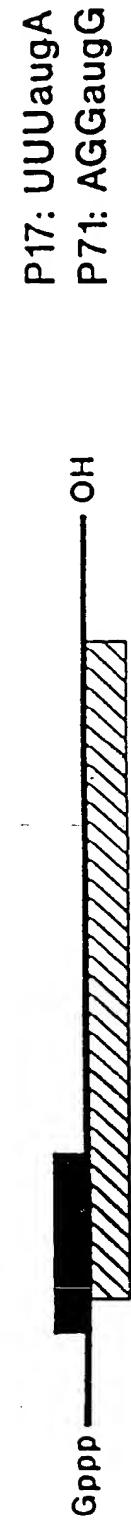
DOT-BLOT DETECTION OF HaSV IN FIELD-COLLECTED
HELICOVERPA LARVAE



09677553-100300

HaSV RNA2

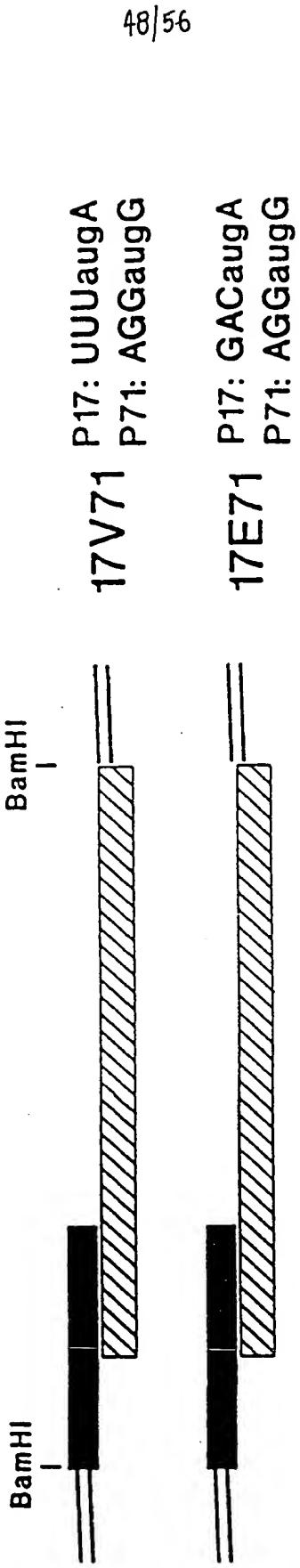
AUG context



P17: UUUa^GA
P71: AGGau^GG

Baculovirus Constructs

BamHI



P17: UUUa^GA
P71: AGGau^GG

P17: GACau^GA
P71: AGGau^GG

P71: GACau^GA

V71 P71: AGGau^GG

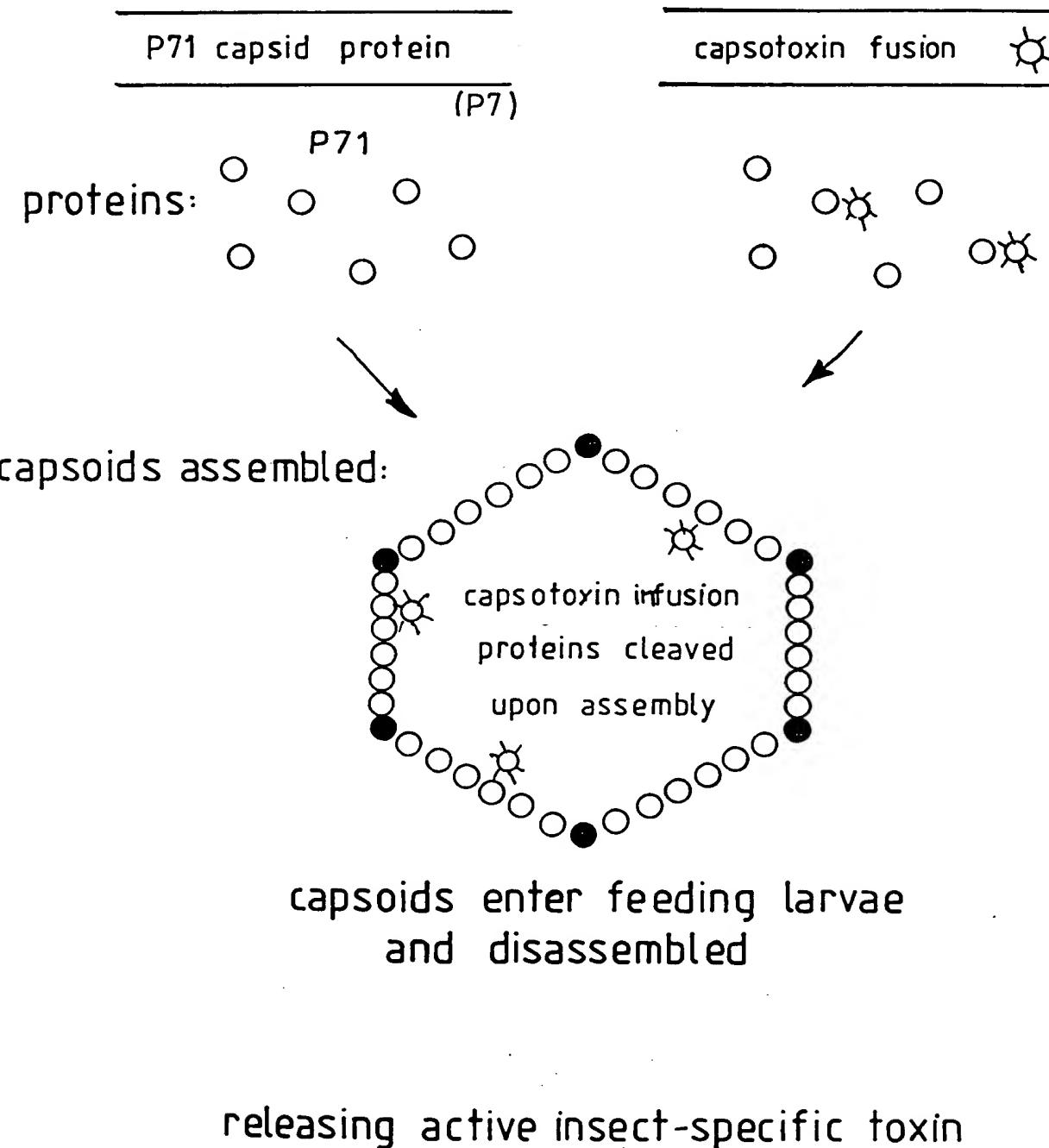
R2 P17: UUUa^GA
P71: AGGau^GG

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III.13.

Virus capsid strategy:
capsotoxin encapsulation

transgenic plant genome:



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Virus capsid strategy: toxin message encapsulation and amplification

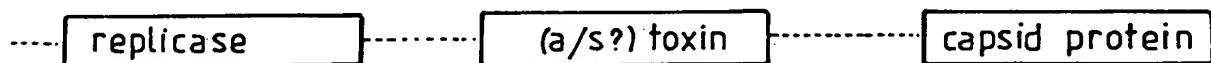
HaSV RNA 1



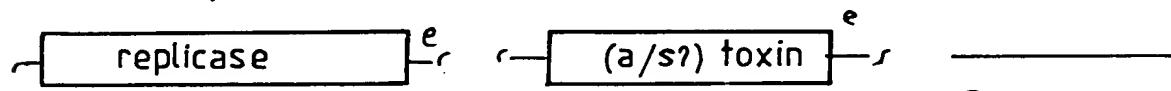
HaSV RNA 2



transgenic plant genome:

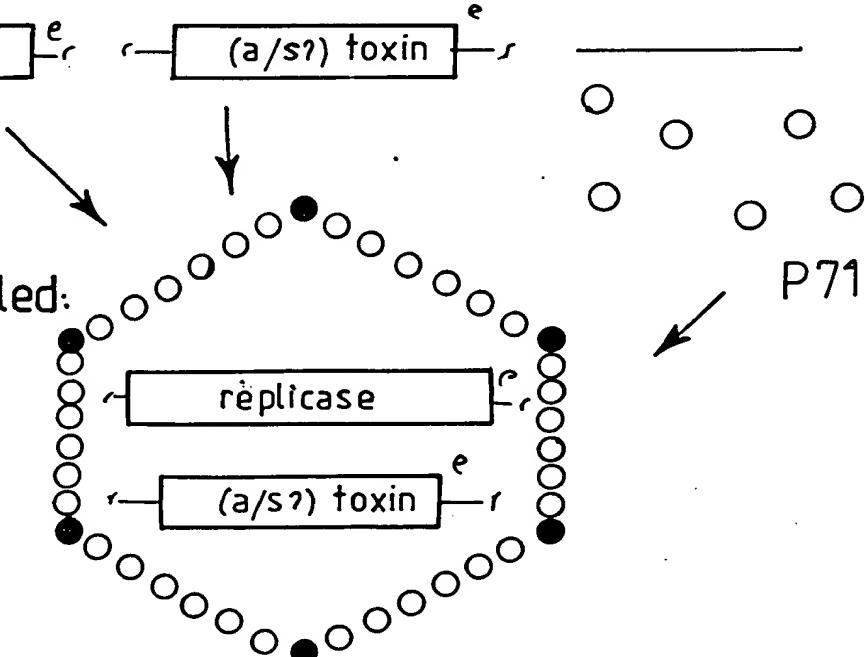


transcripts:



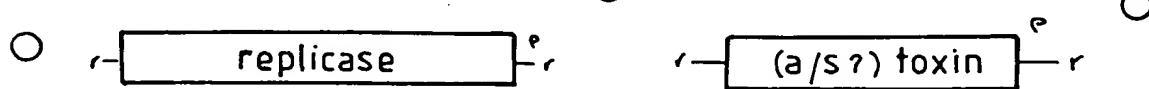
proteins:

capsoids assembled:



capsoids enter and infect feeding larvae

capsoids disassembled:



mRNA amplification and expression and secretion of
toxin

HIG. 14b

Virus expression in plants: the one-way vector

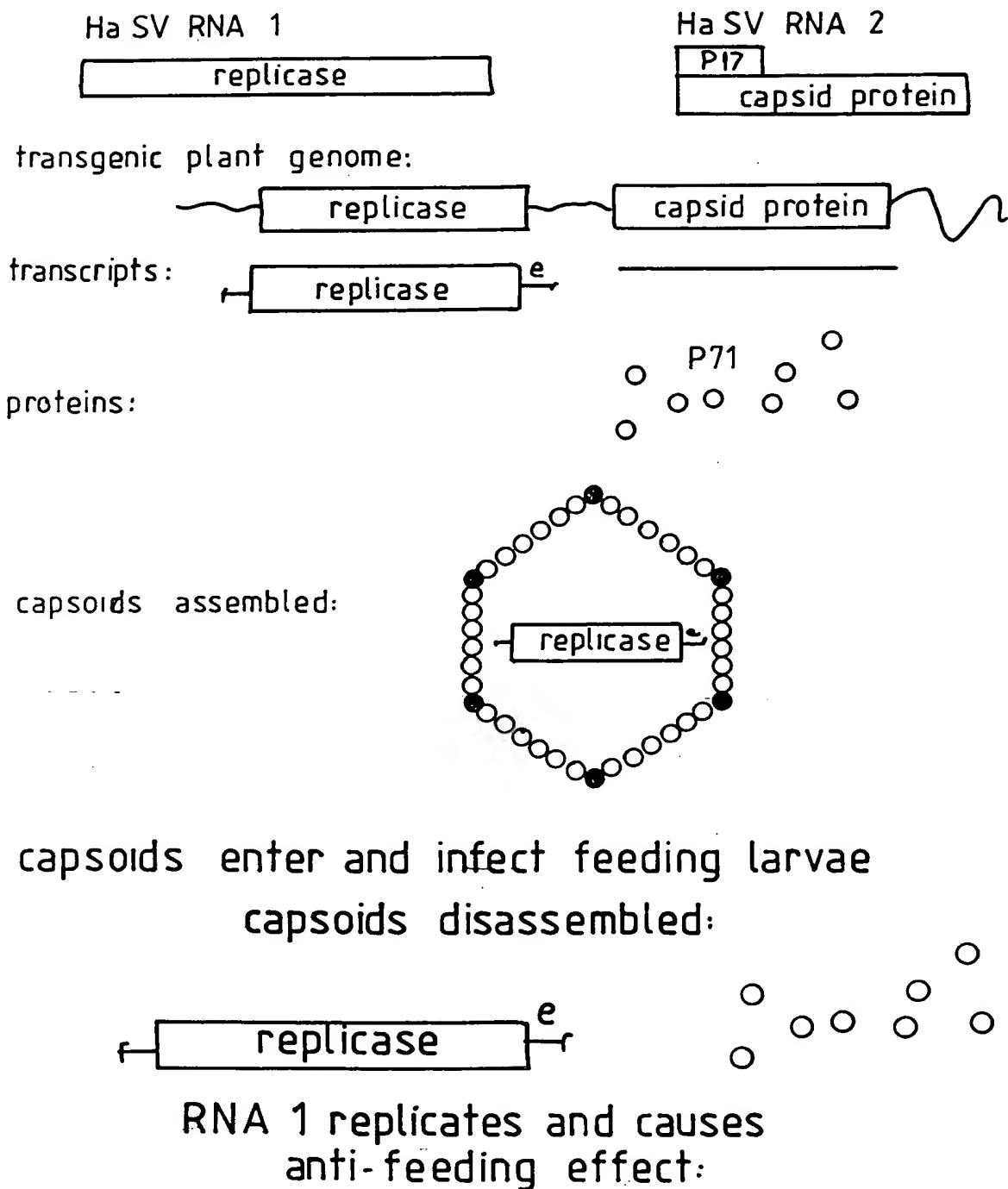


FIG. 14C

HaSV RNA1



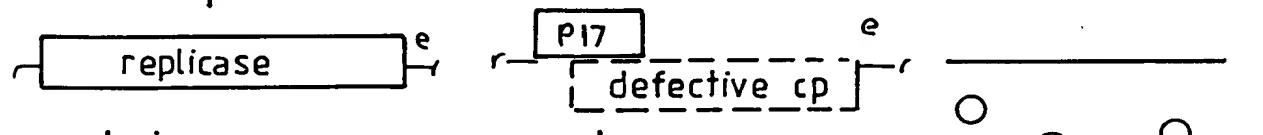
HaSV RNA



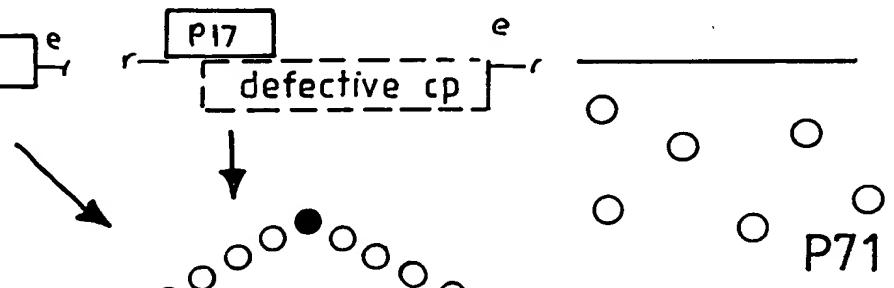
transgenic plant genome:



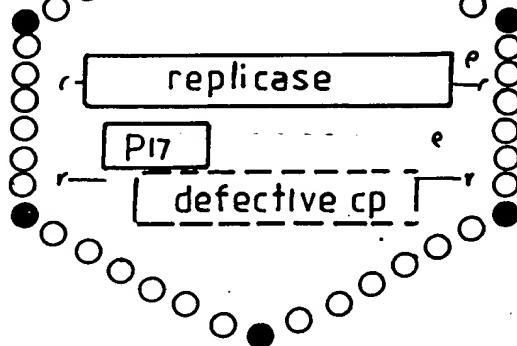
transcripts:



proteins:

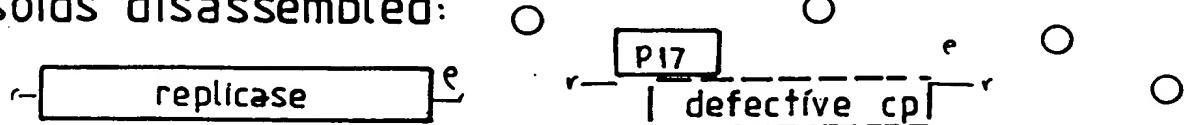


capsoids assembled:



capsoids enter and infect feeding larvae

capsoids disassembled:



viral RNA replicates and causes anti-feeding effect

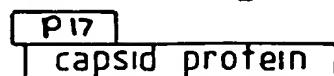
FIG. 14d

Virus expression in plants

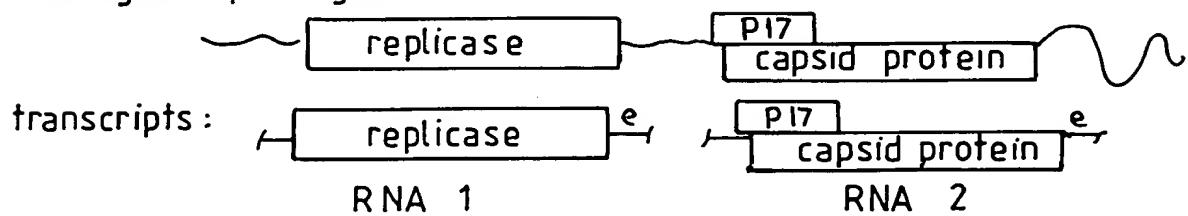
Ha SV RNA 1



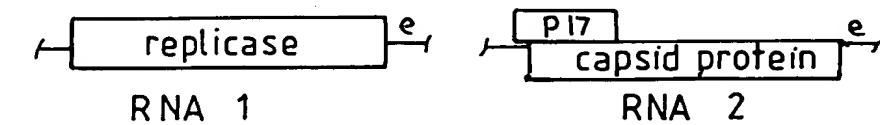
Ha SV RNA 2



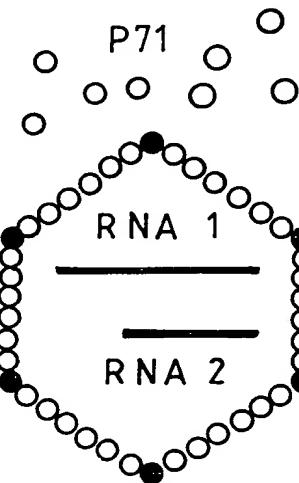
transgenic plant genome:



transcripts:



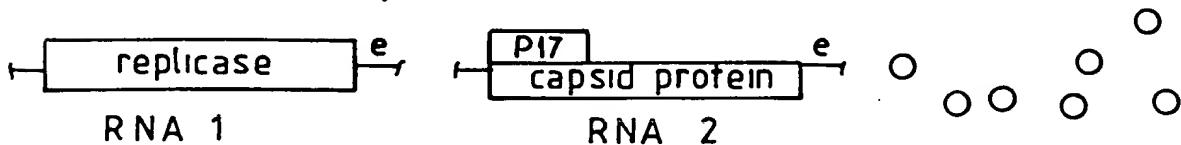
proteins:



capsids assembled:

capsids enter and infect feeding larvae

capsids disassembled:



virus replicates and causes
anti-feeding effect

FIG. 14 e

Virus expression in plants:
the one-way vector for a toxin

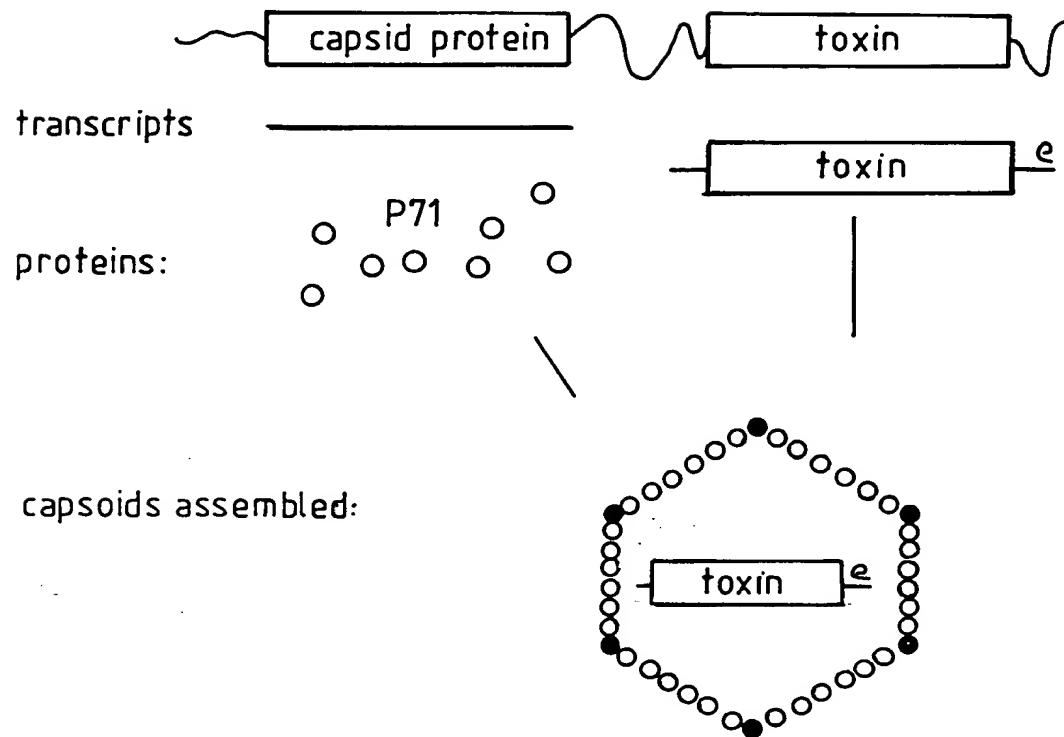
Ha SV RNA 1



Ha SV RNA 2

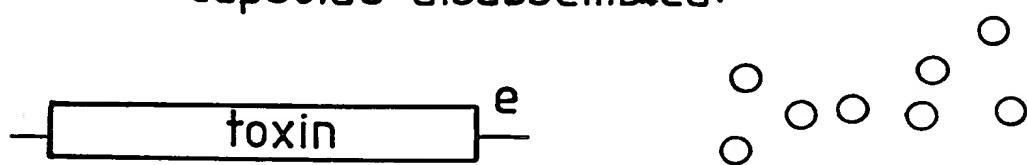


transgenic plant genome:



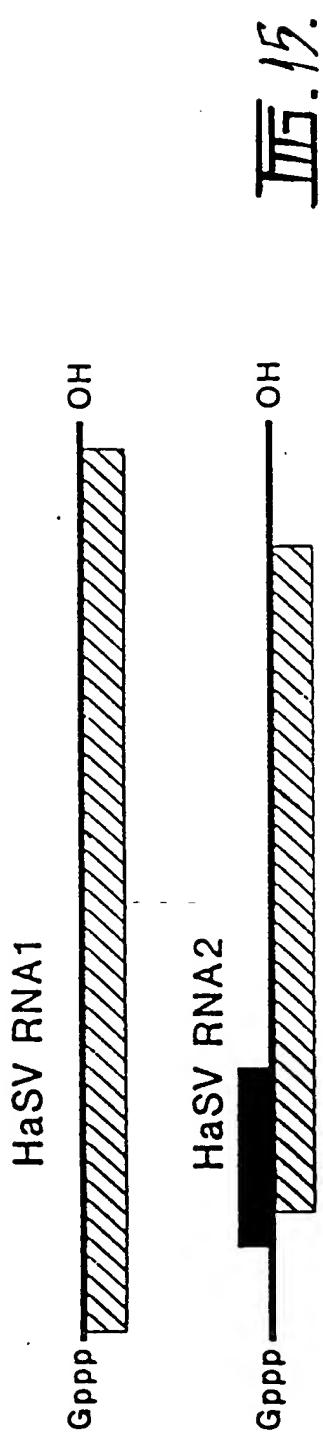
capsoids enter and infect feeding larvae

capsoids disassembled:

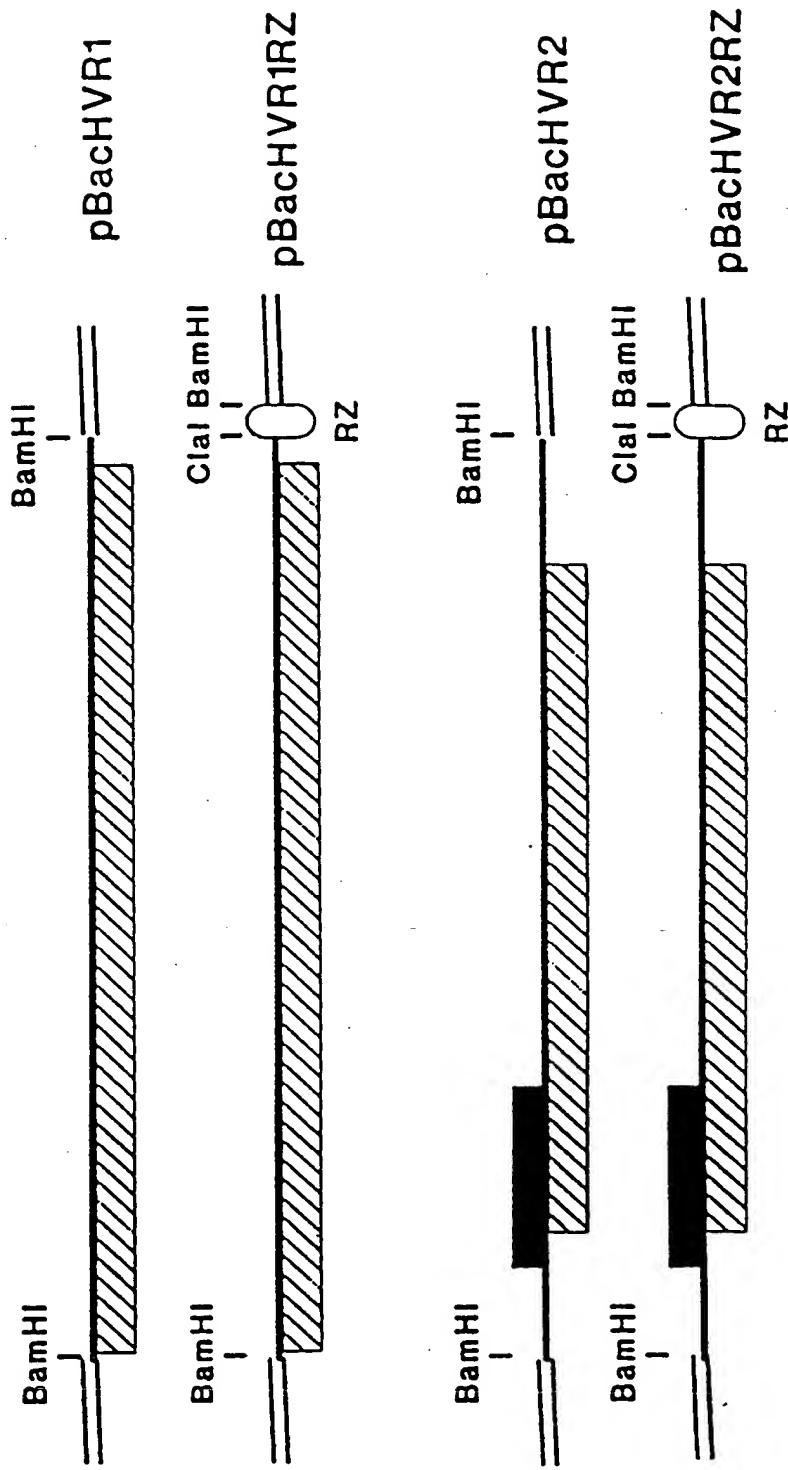


toxin expressed and causes
lavae to cease feeding

III. 14f



baculovirus expression constructs



III. 16.

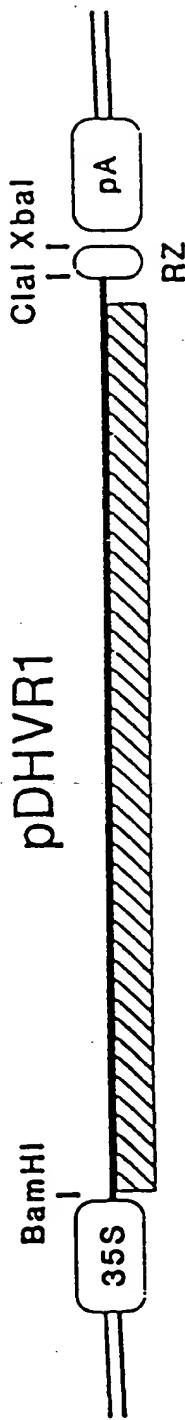
HaSV RNA1



HaSV RNA2



Protoplast expression constructs



pDHVR2

